



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/603,260A

DATE: 08/23/2004

TIME: 10:28:28

Input Set : A:\amended Sequence Listing.txt
Output Set: N:\CRF4\08232004\J603260A.raw



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| | | |
|-----|--|------|
| 78 | tcctgtaaa ccctctccca tgcgtcgcc atcggctcac cttgcaagg agcttccatt | 1860 |
| 80 | gtcaataaaa ttgagcaatt agtttaggg gtggcactag gtaattcagc agaatttggg | 1920 |
| 82 | ttaaaaagaac acgacgacga atccccatcc cacaaaaaat caggcagtat tgcaggaacg | 1980 |
| 84 | ataccttag ggctgcgcag ctttactg cgcatccac tggactccga tggtaaccgtc | 2040 |
| 86 | acagtagaaag aaacaaaaat agctggcatg acagatcata tcgcgatatc caccactca | 2100 |
| 88 | tacgagaatg ctgttaatc attccgttgc cgagcaaatac gaccacttc ttcgttatga | 2160 |
| 90 | ccgcttccgg cgctaaagcc gtttaaactt cagatgatag tgcgttatgt atcaaaccga | 2220 |
| 92 | tggtgattga aaacataaccc accattcatt cagaataaga cggtgccatc atcagagctt | 2280 |
| 94 | tcccatgaa taaacaatcc gcgactttac gtctggccgc tttaactaaa ttggcaagtg | 2340 |
| 96 | tctgccgcga tacgctgatg ccgcataatg aagccagccc cgacacccgc caacacccgc | 2400 |
| 98 | tgacgcgcgc tgacgggctt gtctgtccc ggcatecgct tacagacaag ctgtgaccgt | 2460 |
| 100 | ctccgggagc tgcatgtgtc agaggtttc accgtcatca ccgaaacgcg cgagacgaaa | 2520 |
| 102 | gggcctcgat atacgcctat tttataggt taatgtcatg ataataatgg tttcttag | 2578 |
| 105 | <210> SEQ ID NO: 2 | |
| 106 | <211> LENGTH: 798 | |
| 107 | <212> TYPE: DNA | |
| 108 | <213> ORGANISM: Vibrio metschnikovii RH530 | |
| 110 | <220> FEATURE: | |
| 111 | <221> NAME/KEY: CDS | |
| 112 | <222> LOCATION: (1)..(798) | |
| 113 | <223> OTHER INFORMATION: valL1 gene | |
| 116 | <400> SEQUENCE: 2 | |
| 117 | atg ttt gtc aca aag tct tat tta cat ttg acc atc atc atg cac tta | 48 |
| 118 | Met Phe Val Thr Lys Ser Tyr Leu His Leu Thr Ile Ile Met His Leu | |
| 119 | 1 5 10 15 | |
| 121 | cct aaa ata agc ccg ttg ttt att agg gaa gcc att atg att gtc act | 96 |
| 122 | Pro Lys Ile Ser Pro Leu Phe Ile Arg Glu Ala Ile Met Ile Val Thr | |
| 123 | 20 25 30 | |
| 125 | atc gat atg att tgt ctg cgt ctt gcg ccg aaa tct atc cag gtt tta | 144 |
| 126 | Ile Asp Met Ile Cys Leu Arg Leu Ala Pro Lys Ser Ile Gln Val Leu | |
| 127 | 35 40 45 | |
| 129 | ctg gtg aaa cgc tct aat cca aat ccg cca gat tgt ggt aaa tgg gca | 192 |
| 130 | Leu Val Lys Arg Ser Asn Pro Asn Arg Pro Asp Cys Gly Lys Trp Ala | |
| 131 | 50 55 60 | |
| 133 | ttg cct ggc ggg ata gtg tat gac gaa gat atg acc gct cat ggt gga | 240 |
| 134 | Leu Pro Gly Gly Ile Val Tyr Asp Glu Asp Met Thr Ala His Gly Gly | |
| 135 | 65 70 75 80 | |
| 137 | gaa cct gtc gat gag gat ttt gat gca gcg aga cga cgt att tgt cgg | 288 |
| 138 | Glu Pro Val Asp Glu Asp Phe Asp Ala Ala Arg Arg Arg Ile Cys Arg | |
| 139 | 85 90 95 | |
| 141 | caa aaa gtc cat act tat cct aat ttt atc agc gat ccg ctg gtt gat | 336 |
| 142 | Gln Lys Val His Thr Tyr Pro Asn Phe Ile Ser Asp Pro Leu Val Asp | |
| 143 | 100 105 110 | |
| 145 | ggc aac ccc aaa cgc gat ccg aat ggt tgg agt gtc agt att tcc cat | 384 |
| 146 | Gly Asn Pro Lys Arg Asp Pro Asn Gly Trp Ser Val Ser Ile Ser His | |
| 147 | 115 120 125 | |
| 149 | tac gct tta tta aac ccg tgg aat gtc aaa caa ata gaa gat ttt ggt | 432 |
| 150 | Tyr Ala Leu Leu Asn Pro Trp Asn Val Lys Gln Ile Glu Asp Phe Gly | |
| 151 | 130 135 140 | |

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| | |
|--|-----|
| 153 atc gac ccc gag cgc gct aat tgg ttt gat ctt cat act tta ctc aaa | 480 |
| 154 Ile Asp Pro Glu Arg Ala Asn Trp Phe Asp Leu His Thr Leu Leu Lys | |
| 155 145 150 155 160 | |
| 157 gaa gaa atg ccg ctg gct ttt gat cat gtc gcg caa att cag cat .gcf | 528 |
| 158 Glu Glu Met Pro Leu Ala Phe Asp His Val Ala Gln Ile Gln His Ala | |
| 159 165 170 175 | |
| 161 tgg caa aaa tta cgc gct gcg gtt gaa tac aca tcc gtg gta cta ttt | 576 |
| 162 Trp Gln Lys Leu Arg Ala Ala Val Glu Tyr Thr Ser Val Val Leu Phe | |
| 163 180 185 190 | |
| 165 tca tta gaa aaa gag ttt tta gtg gcg gat att att gat gcc tac gcc | 624 |
| 166 Ser Leu Glu Lys Glu Phe Leu Val Ala Asp Ile Ile Asp Ala Tyr Ala | |
| 167 195 200 205 | |
| 169 aaa ttt ggc gtc gaa gtt aat cgc atg acc att aaa cgc cgc ttg atc | 672 |
| 170 Lys Phe Gly Val Glu Val Asn Arg Met Thr Ile Lys Arg Arg Leu Ile | |
| 171 210 215 220 | |
| 173 aat acc ggg gtg atc gtc agt acc aat aaa atg gcc gca tct tgt aaa | 720 |
| 174 Asn Thr Gly Val Ile Val Ser Thr Asn Lys Met Ala Ala Ser Cys Lys | |
| 175 225 230 235 240 | |
| 177 ggc aaa gga gcc aaa cca gcc acc gtt tat cgt ctt gcc agt cat gaa | 768 |
| 178 Gly Lys Gly Ala Lys Pro Ala Thr Val Tyr Arg Leu Ala Ser His Glu | |
| 179 245 250 255 | |
| 181 gtc acc tat ttt caa acc tgt tta cga ggt | 798 |
| 182 Val Thr Tyr Phe Gln Thr Cys Leu Arg Gly | |
| 183 260 265 | |
| 186 <210> SEQ ID NO: 3 | |
| 187 <211> LENGTH: 266 | |
| 188 <212> TYPE: PRT | |
| 189 <213> ORGANISM: Vibrio metschnikovii RH530 | |
| 191 <400> SEQUENCE: 3 | |
| 192 Met Phe Val Thr Lys Ser Tyr Leu His Leu Thr Ile Ile Met His Leu | |
| 193 1 5 10 15 | |
| 195 Pro Lys Ile Ser Pro Leu Phe Ile Arg Glu Ala Ile Met Ile Val Thr | |
| 196 20 25 30 | |
| 198 Ile Asp Met Ile Cys Leu Arg Leu Ala Pro Lys Ser Ile Gln Val Leu | |
| 199 35 40 45 | |
| 201 Leu Val Lys Arg Ser Asn Pro Asn Arg Pro Asp Cys Gly Lys Trp Ala | |
| 202 50 55 60 | |
| 204 Leu Pro Gly Gly Ile Val Tyr Asp Glu Asp Met Thr Ala His Gly Gly | |
| 205 65 70 75 80 | |
| 207 Glu Pro Val Asp Glu Asp Phe Asp Ala Ala Arg Arg Arg Ile Cys Arg | |
| 208 85 90 95 | |
| 210 Gln Lys Val His Thr Tyr Pro Asn Phe Ile Ser Asp Pro Leu Val Asp | |
| 211 100 105 110 | |
| 213 Gly Asn Pro Lys Arg Asp Pro Asn Gly Trp Ser Val Ser Ile Ser His | |
| 214 115 120 125 | |
| 216 Tyr Ala Leu Leu Asn Pro Trp Asn Val Lys Gln Ile Glu Asp Phe Gly | |
| 217 130 135 140 | |
| 219 Ile Asp Pro Glu Arg Ala Asn Trp Phe Asp Leu His Thr Leu Leu Lys | |
| 220 145 150 155 160 | |

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222 Glu Glu Met Pro Leu Ala Phe Asp His Val Ala Gln Ile Gln His Ala
 223 165 170 175
 225 Trp Gln Lys Leu Arg Ala Ala Val Glu Tyr Thr Ser Val Val Leu Phe
 226 180 185 190
 228 Ser Leu Glu Lys Glu Phe Leu Val Ala Asp Ile Ile Asp Ala Tyr Ala
 229 195 200 205
 231 Lys Phe Gly Val Glu Val Asn Arg Met Thr Ile Lys Arg Arg Leu Ile
 232 210 215 220
 234 Asn Thr Gly Val Ile Val Ser Thr Asn Lys Met Ala Ala Ser Cys Lys
 235 225 230 235 240
 237 Gly Lys Gly Ala Lys Pro Ala Thr Val Tyr Arg Leu Ala Ser His Glu
 238 245 250 255
 240 Val Thr Tyr Phe Gln Thr Cys Leu Arg Gly
 241 260 265
 244 <210> SEQ ID NO: 4
 245 <211> LENGTH: 555
 246 <212> TYPE: DNA
 247 <213> ORGANISM: Vibrio metschnikovii RH530
 249 <220> FEATURE:
 250 <221> NAME/KEY: CDS
 251 <222> LOCATION: (1)..(555)
 252 <223> OTHER INFORMATION: valL2 gene
 255 <400> SEQUENCE: 4
 256 atg cag att att ctt gtt cat gga ctc tat atg cat ggc ttg gta atg 48
 257 Met Gln Ile Ile Leu Val His Gly Leu Tyr Met His Gly Leu Val Met
 258 1 5 10 15
 260 cat ccg ctt agt cat cgt ctg cat aaa ttg ggt tat cgt act caa acc 96
 261 His Pro Leu Ser His Arg Leu His Lys Leu Gly Tyr Arg Thr Gln Thr
 262 20 25 30
 264 att agc tac aac tca ctc gct atc gat gat gag gcc att ttt cgc cgc 144
 265 Ile Ser Tyr Asn Ser Leu Ala Ile Asp Asp Glu Ala Ile Phe Arg Arg
 266 35 40 45
 268 ctt gac cga tcg ctc act cat gcc tcg cct aat gct tta gtc gga cac 192
 269 Leu Asp Arg Ser Leu Thr His Ala Ser Pro Asn Ala Leu Val Gly His
 270 50 55 60
 272 agt ttg ggc gga ttg gtg atc aaa cgt tat cta gaa tcg cgc gca ccg 240
 273 Ser Leu Gly Gly Leu Val Ile Lys Arg Tyr Leu Glu Ser Arg Ala Pro
 274 65 70 75 80
 276 tcc tgt gaa acc ctc tcc cat gtc gtc gcc atc ggc tca cct ttg caa 288
 277 Ser Cys Glu Thr Leu Ser His Val Val Ala Ile Gly Ser Pro Leu Gln
 278 85 90 95
 280 gga gct tcc att gtc aat aaa att gagcaa tta ggt tta ggg gtg gca 336
 281 Gly Ala Ser Ile Val Asn Lys Ile Glu Gln Leu Gly Leu Gly Val Ala
 282 100 105 110
 284 cta ggt aat tca gca gaa ttt ggg tta aaa gaa cac gac gac gaa tcc 384
 285 Leu Gly Asn Ser Ala Glu Phe Gly Leu Lys Glu His Asp Asp Glu Ser
 286 115 120 125
 288 cgc tat cca caa aaa tca ggc agt att gca gga acg ata cct tta ggg 432
 289 Arg Tyr Pro Gln Lys Ser Gly Ser Ile Ala Gly Thr Ile Pro Leu Gly

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| | | | | | | | | | | | | | | | | | |
|-----|-------|------------|----------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 290 | 130 | 135 | 140 | | | | | | | | | | | | | | |
| 292 | ctg | cgc | acc | gtc | | | | | | | | | | | | | |
| 293 | Leu | Arg | Ser | Leu | Leu | Arg | Asp | Pro | Leu | Asp | Ser | Asp | Gly | Thr | Val | 480 | |
| 294 | 145 | | | 150 | | 155 | | | 160 | | | | | | | | |
| 296 | aca | gta | gaa | gaa | acc | aaa | ata | gct | ggc | atg | aca | gat | cat | atc | gcg | ata | 528 |
| 297 | Thr | Val | Glu | Glu | Thr | Lys | Ile | Ala | Gly | Met | Thr | Asp | His | Ile | Ala | Ile | |
| 298 | | | | 165 | | 170 | | | | 175 | | | | | | | |
| 300 | tcc | acc | act | tca | tac | gag | aat | gct | gtt | | | | | | | | 555 |
| 301 | Ser | Thr | Thr | Ser | Tyr | Glu | Asn | Ala | Val | | | | | | | | |
| 302 | | | | 180 | | 185 | | | | | | | | | | | |
| 305 | <210> | SEQ ID NO: | 5 | | | | | | | | | | | | | | |
| 306 | <211> | LENGTH: | 185 | | | | | | | | | | | | | | |
| 307 | <212> | TYPE: | PRT | | | | | | | | | | | | | | |
| 308 | <213> | ORGANISM: | Vibrio metschnikovii RH530 | | | | | | | | | | | | | | |
| 310 | <400> | SEQUENCE: | 5 | | | | | | | | | | | | | | |
| 311 | Met | Gln | Ile | Ile | Leu | Val | His | Gly | Leu | Tyr | Met | His | Gly | Leu | Val | Met | |
| 312 | 1 | | | | 5 | | | | 10 | | | | | 15 | | | |
| 314 | His | Pro | Leu | Ser | His | Arg | Leu | His | Lys | Leu | Gly | Tyr | Arg | Thr | Gln | Thr | |
| 315 | | | | | 20 | | | | 25 | | | | | 30 | | | |
| 317 | Ile | Ser | Tyr | Asn | Ser | Leu | Ala | Ile | Asp | Asp | Glu | Ala | Ile | Phe | Arg | Arg | |
| 318 | | | | | 35 | | | | 40 | | | | 45 | | | | |
| 320 | Leu | Asp | Arg | Ser | Leu | Thr | His | Ala | Ser | Pro | Asn | Ala | Leu | Val | Gly | His | |
| 321 | | | | | 50 | | | | 55 | | | 60 | | | | | |
| 323 | Ser | Leu | Gly | Gly | Leu | Val | Ile | Lys | Arg | Tyr | Leu | Glu | Ser | Arg | Ala | Pro | |
| 324 | 65 | | | | | 70 | | | 75 | | | | 80 | | | | |
| 326 | Ser | Cys | Glu | Thr | Leu | Ser | His | Val | Val | Ala | Ile | Gly | Ser | Pro | Leu | Gln | |
| 327 | | | | | | 85 | | | 90 | | | | 95 | | | | |
| 329 | Gly | Ala | Ser | Ile | Val | Asn | Lys | Ile | Glu | Gln | Leu | Gly | Leu | Gly | Val | Ala | |
| 330 | | | | | 100 | | | | 105 | | | 110 | | | | | |
| 332 | Leu | Gly | Asn | Ser | Ala | Glu | Phe | Gly | Leu | Lys | Glu | His | Asp | Asp | Glu | Ser | |
| 333 | | | | | 115 | | | | 120 | | | 125 | | | | | |
| 335 | Arg | Tyr | Pro | Gln | Lys | Ser | Gly | Ser | Ile | Ala | Gly | Thr | Ile | Pro | Leu | Gly | |
| 336 | | | | | 130 | | | | 135 | | | 140 | | | | | |
| 338 | Leu | Arg | Ser | Leu | Leu | Leu | Arg | Asp | Pro | Leu | Asp | Ser | Asp | Gly | Thr | Val | |
| 339 | 145 | | | | | 150 | | | | 155 | | | 160 | | | | |
| 341 | Thr | Val | Glu | Glu | Thr | Lys | Ile | Ala | Gly | Met | Thr | Asp | His | Ile | Ala | Ile | |
| 342 | | | | | | 165 | | | 170 | | | 175 | | | | | |
| 344 | Ser | Thr | Thr | Ser | Tyr | Glu | Asn | Ala | Val | | | | | | | | |
| 345 | | | | | 180 | | | | 185 | | | | | | | | |
| 348 | <210> | SEQ ID NO: | 6 | | | | | | | | | | | | | | |
| 349 | <211> | LENGTH: | 117 | | | | | | | | | | | | | | |
| 350 | <212> | TYPE: | PRT | | | | | | | | | | | | | | |
| 351 | <213> | ORGANISM: | Pseudomonas glumae | | | | | | | | | | | | | | |
| 353 | <400> | SEQUENCE: | 6 | | | | | | | | | | | | | | |
| 354 | Val | Ala | Asn | Leu | Ser | Gly | Phe | Gln | Ser | Asp | Asp | Gly | Pro | Asn | Gly | Arg | |
| 355 | 1 | | | | 5 | | | | 10 | | | 15 | | | | | |
| 357 | Gly | Glu | Gln | Leu | Leu | Ala | Tyr | Val | Lys | Gln | Val | Leu | Ala | Thr | Thr | Gly | |
| 358 | | | | | 20 | | | | 25 | | | 30 | | | | | |
| 360 | Ala | Thr | Lys | Val | Asn | Leu | Ile | Gly | His | Ser | Gln | Gly | Gly | Leu | Thr | Ser | |

VERIFICATION SUMMARY DATE: 08/23/2004
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L:8 M:270 C: Current Application Number differs, Replaced Current Application No
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE